

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 21:15:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716154.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716154 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716154.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 21:15:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716154.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,460,850
Mapped reads	10,500,284 / 91.62%
Unmapped reads	960,566 / 8.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,118 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	1,153,434 / 10.06%
Duplication rate	8%
Clipped reads	10,522,518 / 91.81%

2.2. ACGT Content

Number/percentage of A's	145,351,190 / 24.04%
Number/percentage of C's	111,596,858 / 18.46%
Number/percentage of T's	194,629,557 / 32.2%
Number/percentage of G's	152,923,227 / 25.3%
Number/percentage of N's	13,517 / 0%
GC Percentage	43.76%

2.3. Coverage

Mean	0.1953

Standard Deviation	1.185
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2.4. Mapping Quality

Mean Mapping Quality	45.24
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2.5. Mismatches and indels

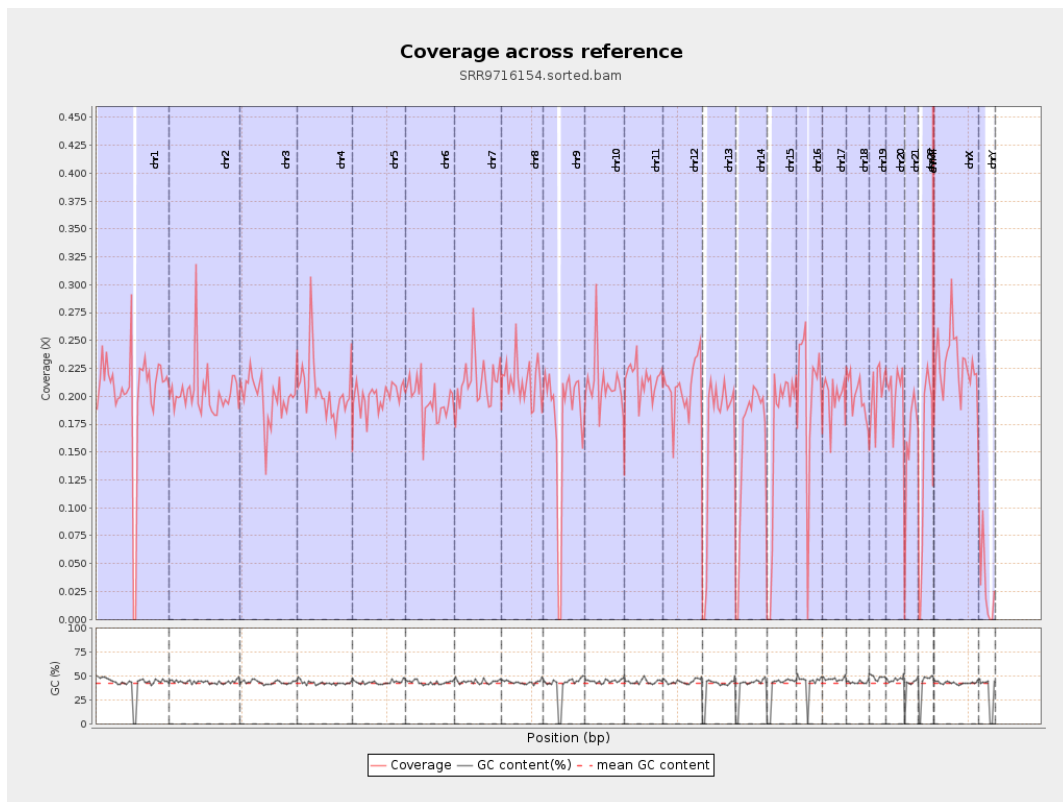
General error rate	0.49%
Mismatches	2,902,137
Insertions	36,733
Mapped reads with at least one insertion	0.35%
Deletions	87,766
Mapped reads with at least one deletion	0.83%
Homopolymer indels	42.34%

2.6. Chromosome stats

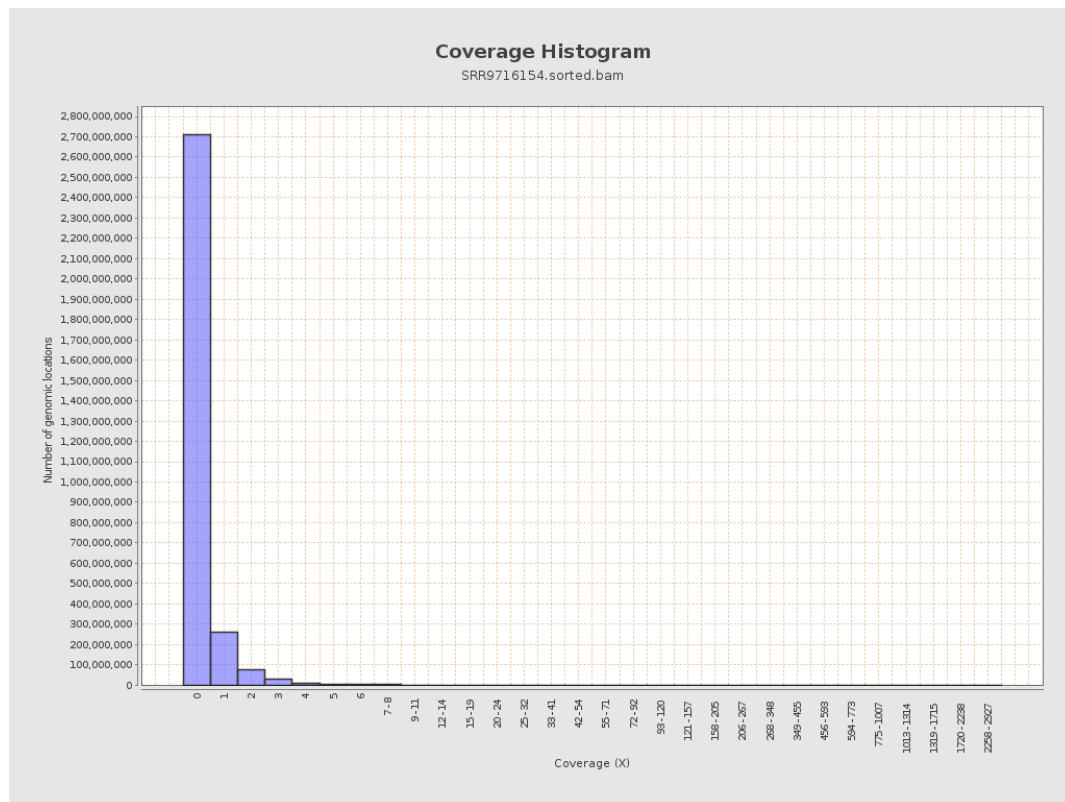
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	50336893	0.202	2.3305
chr2	243199373	49595973	0.2039	1.3418
chr3	198022430	39447031	0.1992	0.6669
chr4	191154276	39234589	0.2053	0.8338
chr5	180915260	36144350	0.1998	0.6803
chr6	171115067	33541476	0.196	0.7739
chr7	159138663	34024255	0.2138	1.3337

chr8	146364022	31321914	0.214	1.0935
chr9	141213431	25162289	0.1782	1.1787
chr10	135534747	28561884	0.2107	1.1254
chr11	135006516	28934341	0.2143	1.1763
chr12	133851895	27770039	0.2075	0.707
chr13	115169878	18965779	0.1647	0.5944
chr14	107349540	17175921	0.16	0.7084
chr15	102531392	16893314	0.1648	0.6142
chr16	90354753	18510031	0.2049	0.8151
chr17	81195210	16160342	0.199	0.7818
chr18	78077248	15652353	0.2005	2.3814
chr19	59128983	12050114	0.2038	1.5446
chr20	63025520	12830720	0.2036	0.738
chr21	48129895	7647380	0.1589	0.7712
chr22	51304566	7246002	0.1412	0.5593
chrMT	16571	92830	5.602	4.5173
chrX	155270560	35588856	0.2292	0.952
chrY	59373566	1775520	0.0299	0.5611

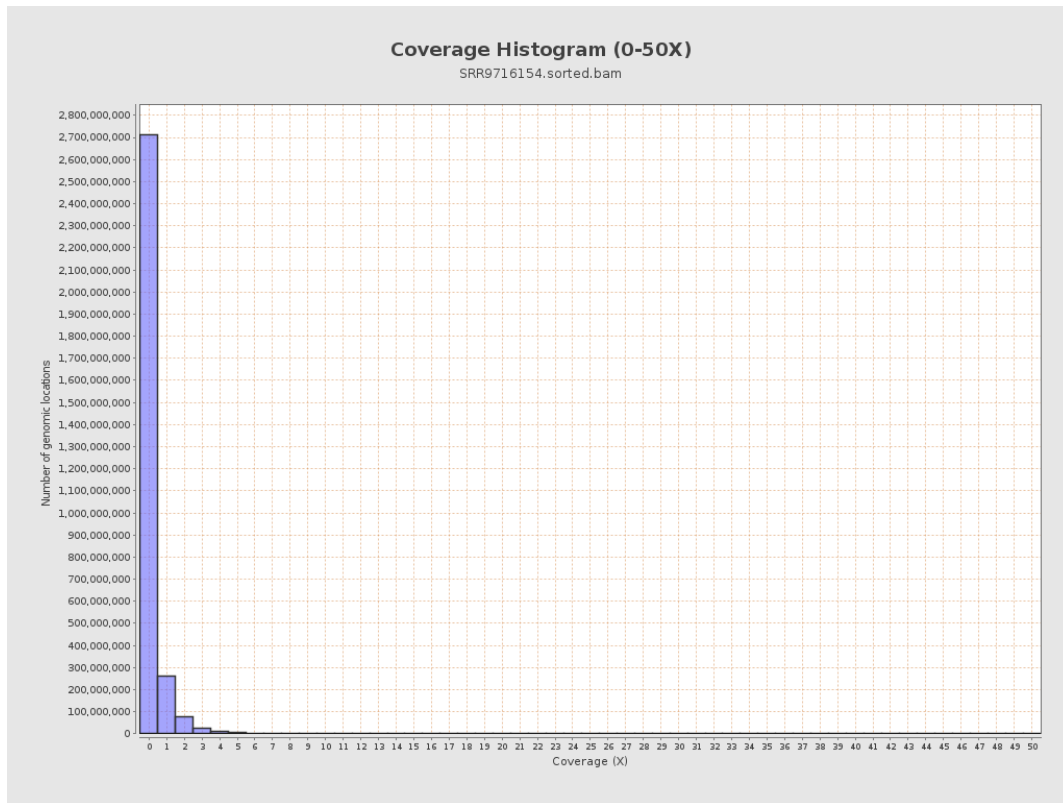
3. Results : Coverage across reference



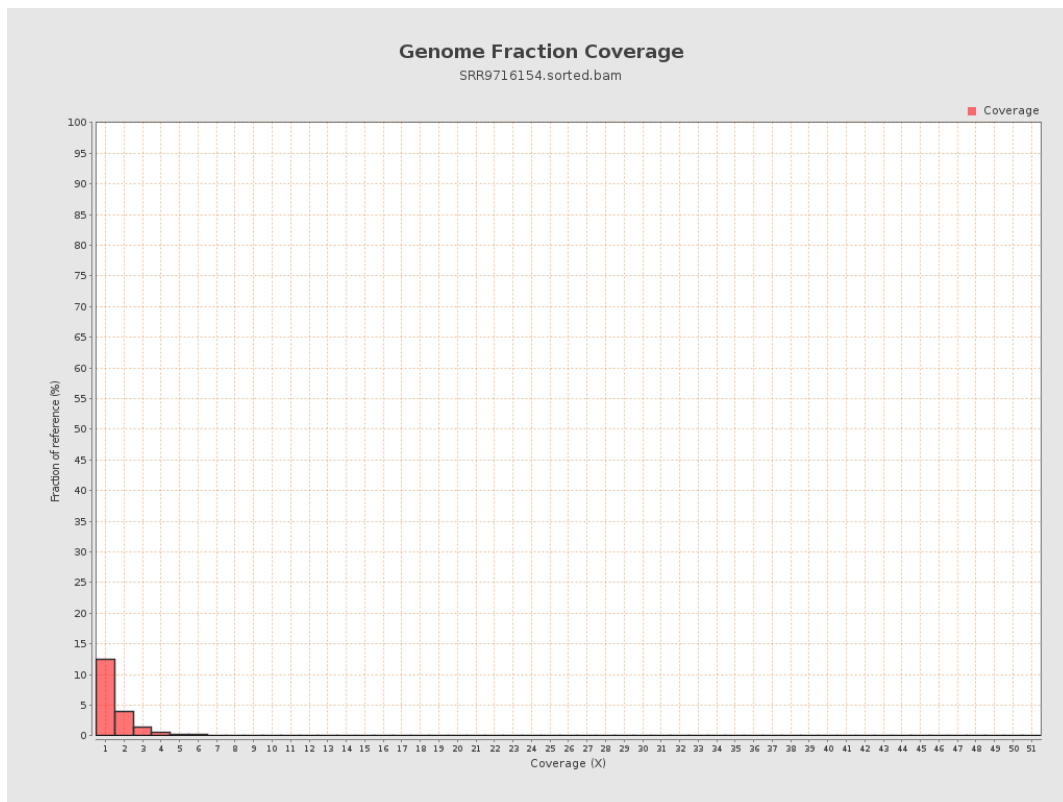
4. Results : Coverage Histogram



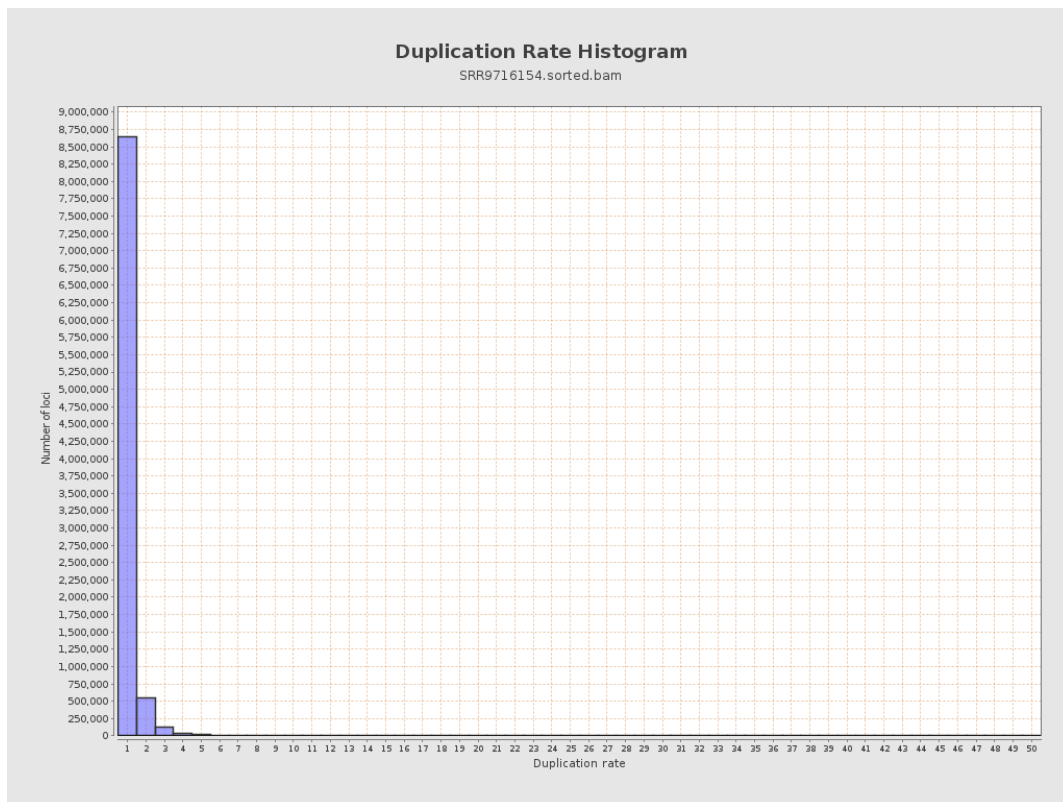
5. Results : Coverage Histogram (0-50X)



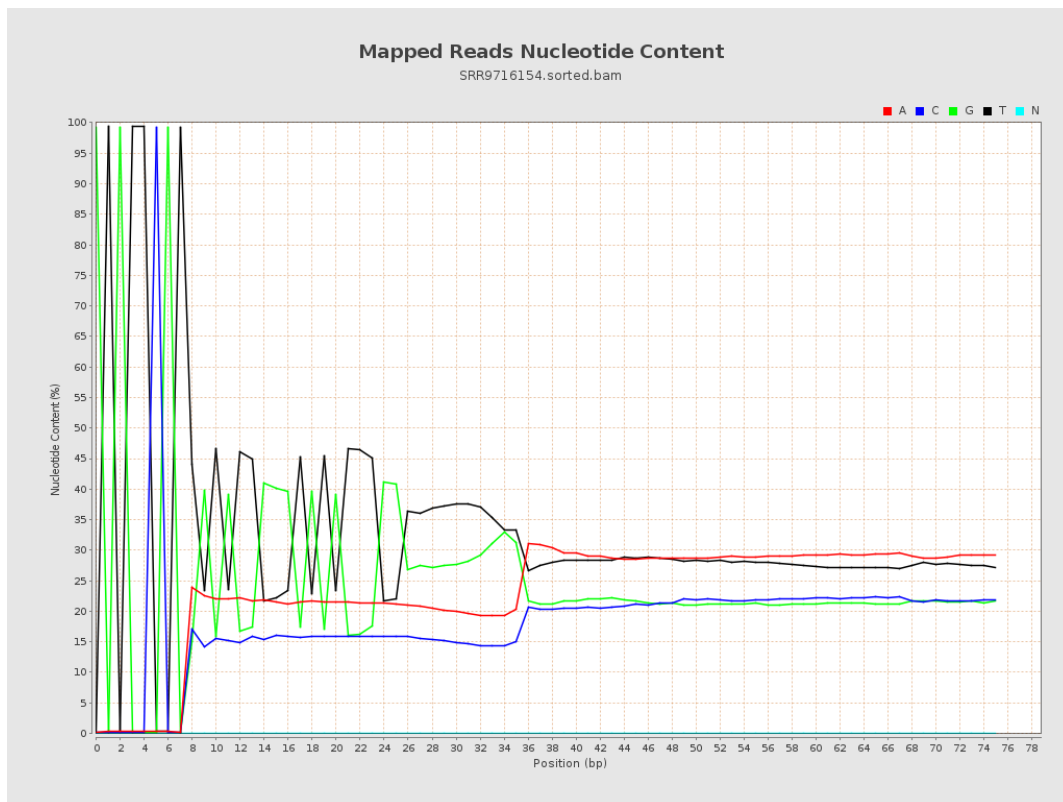
6. Results : Genome Fraction Coverage



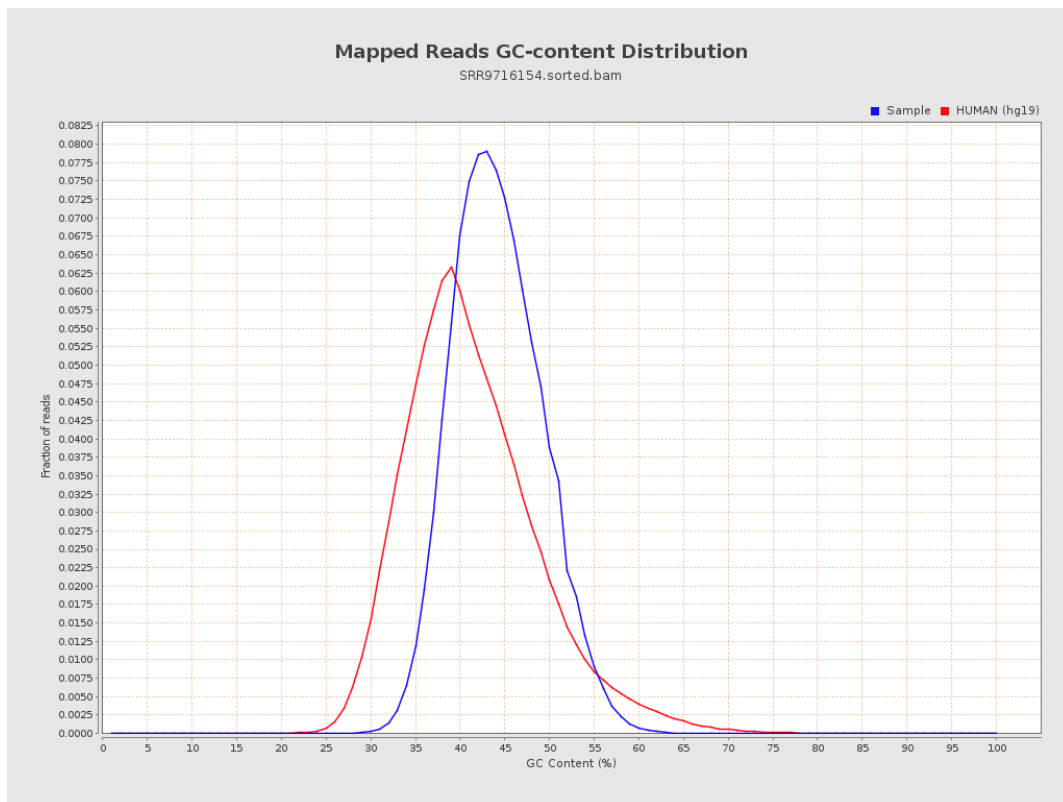
7. Results : Duplication Rate Histogram



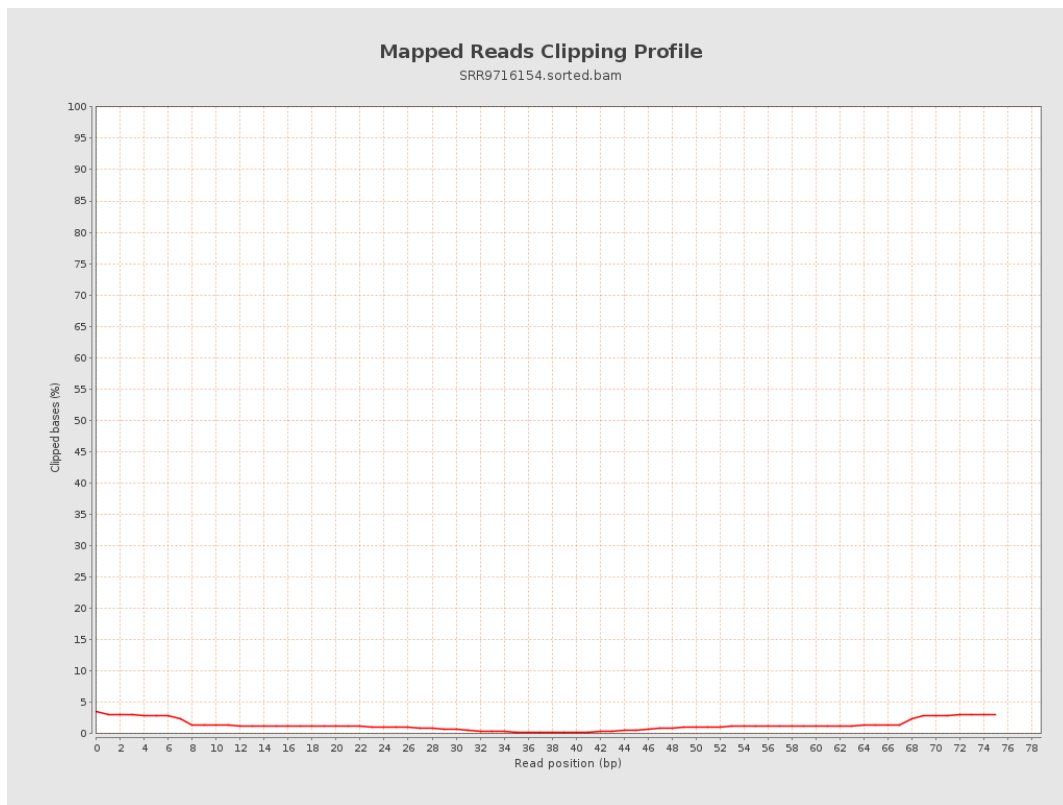
8. Results : Mapped Reads Nucleotide Content



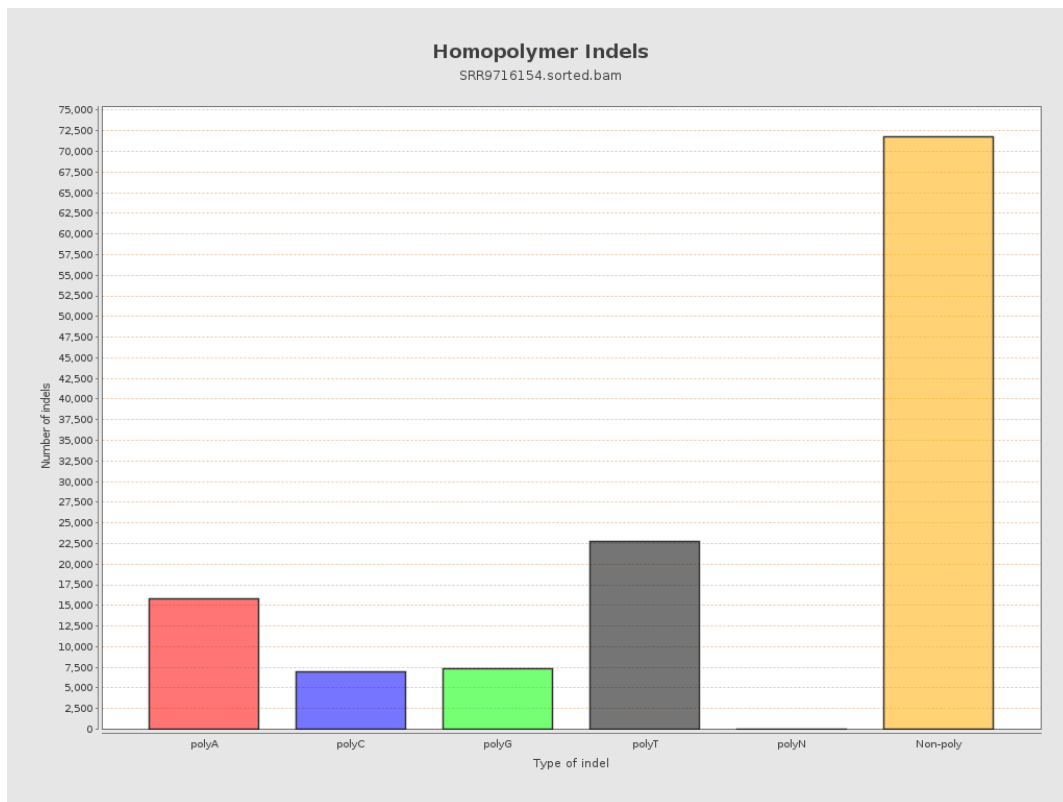
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

